BIOTECͷNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/779, 050*

Source: *OIPE*

Date Processed by STIC: *3/7/2001*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/779,050_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

5(maybe more)

6 _√_ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

Does Not Comply
Corrected Diskette Needed

ρ 6

```
   3 <110> APPLICANT: BOYLE, WILLIAM
   4        HSU, HAILING
   6 <120> TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
   8 <130> FILE REFERENCE: A-570B
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/779,050
  11 <141> CURRENT FILING DATE: 2001-02-12
  13 <150> PRIOR APPLICATION NUMBER: 60/181,800
  14 <151> PRIOR FILING DATE: 2000-02-11
  16 <160> NUMBER OF SEQ ID NOS: 52
  18 <170> SOFTWARE: PatentIn version 3.0
  20 <210> SEQ ID NO: 1
  21 <211> LENGTH: 1173
  22 <212> TYPE: DNA
  23 <213> ORGANISM: Homo sapiens
  25 <220> FEATURE:
  26 <221> NAME/KEY: CDS
  27 <222> LOCATION: (143)..(997)
  29 <400> SEQUENCE: 1
  30 gaattcggca cgagctgagg ggtgagccaa gccctgccat gtagtgcacg caggacatca     60
  32 acaaacacag ataacaggaa atgatccatt ccctgtggtc acttattcta aaggccccaa    120
  34 ccttcaaagt tcaagtagtg at atg gat gac tcc aca gaa agg gag cag tca      172
  35                        Met Asp Asp Ser Thr Glu Arg Glu Gln Ser
  36                         1               5                   10
  38 cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag gag      220
  39 Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys Glu
  40               15                  20                  25
  42 tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc tcc      268
  43 Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser Ser
  44               30                  35                  40
  46 aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg tct      316
  47 Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser
  48               45                  50                  55
  50 tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa ggg      364
  51 Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly
  52       60                  65                  70
  54 gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag aag      412
  55 Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu Lys
  56 75                  80                  85                  90
  58 ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg gag gaa gct cca      460
  59 Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro
  60                   95                  100                 105
  62 gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga gaa      508
  63 Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu
  64                   110                 115                 120
  66 ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt cca      556
  67 Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly Pro
  68             125                 130                 135
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/779,050

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

```
70  gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt gaa     604
71  Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu
72      140                 145                 150
74  aca cca act ata caa aaa gga tct tac aca ttt gtt cca tgg ctt ctc     652
75  Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu
76  155                 160                 165                 170
78  agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag aat aaa ata ttg     700
79  Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu
80              175                 180                 185
82  gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag gtt tta tat act     748
83  Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr
84              190                 195                 200
86  gat aag acc tac gcc atg gga cat cta att cag agg aag aag gtc cat     796
87  Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val His
88              205                 210                 215
90  gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att caa     844
91  Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln
92      220                 225                 230
94  aat atg cct gaa aca cta ccc aat aat tcc tgc tat tca gct ggc att     892
95  Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile
96  235                 240                 245                 250
98  gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca ata cca aga gaa     940
99  Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu
100             255                 260                 265
102 aat gca caa ata tca ctg gat gga gat gtc aca ttt ttt ggt gca ttg     988
103 Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala Leu
104             270                 275                 280
106 aaa ctg ctg tgacctactt acaccatgtc tgtagctatt ttcctccctt            1037
107 Lys Leu Leu
108         285
110 tctctgtacc tctaagaaga aagaatctaa ctgaaaatac caaaaaaaaa aaaaaaaaaa   1097
112 aaaaaaaagt agttaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   1157
114 aaaaactcgg aggggg                                                  1173
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 285
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
122 <400> SEQUENCE: 2
124 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
125 1               5                   10                  15
128 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
129             20                  25                  30
132 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
133         35                  40                  45
136 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
137     50                  55                  60
140 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
141 65                  70                  75                  80
144 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
```

```
145                     85                    90                          95
148 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
149                    100                   105                   110
152 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
153             115                   120                   125
156 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
157        130                   135                   140
160 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
161 145                   150                   155                   160
164 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
165                    165                   170                   175
168 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
169             180                   185                   190
172 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
173             195                   200                   205
176 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
177        210                   215                   220
180 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
181 225                   230                   235                   240
184 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
185             245                   250                   255
188 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
189             260                   265                   270
192 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
193        275                   280                   285
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 1139
198 <212> TYPE: DNA
199 <213> ORGANISM: Mus musculus
201 <220> FEATURE:
202 <221> NAME/KEY: CDS
203 <222> LOCATION: (52)..(978)
205 <400> SEQUENCE: 3
206 gaattcggca cgagctccaa aggcctagac cttcaaagtg ctcctcgtgg a atg gat        57
207                                                             Met Asp
208                                                              1
210 gag tct gca aag acc ctg cca cca ccg tgc ctc tgt ttt tgc tcc gag       105
211 Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys Ser Glu
212          5                  10                  15
214 aaa gga gaa gat atg aaa gtg gga tat gat ccc atc act ccg cag aag       153
215 Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro Gln Lys
216      20                  25                  30
218 gag gag ggt gcc tgg ttt ggg atc tgc agg gat gga agg ctg ctg gct      201
219 Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu Leu Ala
220 35                  40                  45                  50
222 gct acc ctc ctg ctg gcc ctg ttg tcc agc agt ttc aca gcg atg tcc      249
223 Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala Met Ser
224                  55                  60                  65
226 ttg tac cag ttg gct gcc ttg caa gca gac ctg atg aac ctg cgc atg      297
```

```
227 Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu Arg Met
228             70              75                  80
230 gag ctg cag agc tac cga ggt tca gca aca cca gcc gcc gcg ggt gct     345
231 Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala Gly Ala
232             85              90                  95
234 cca gag ttg acc gct gga gtc aaa ctc ctg aca ccg gca gct cct cga     393
235 Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala Pro Arg
236     100             105                 110
238 ccc cac aac tcc agc cgc ggc cac agg aac aga cgc gct ttc cag gga     441
239 Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe Gln Gly
240 115             120                 125                 130
242 cca gag gaa aca gaa caa gat gta gac ctc tca gct cct cct gca cca     489
243 Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro Ala Pro
244             135                 140                 145
246 tgc ctg cct gga tgc cgc cat tct caa cat gat gat aat gga atg aac     537
247 Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly Met Asn
248             150                 155                 160
250 ctc aga aac atc att caa gac tgt ctg cag ctg att gca gac agc gac     585
251 Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Asp
252             165                 170                 175
254 acg ccg act ata cga aaa gga act tac aca ttt gtt cca tgg ctt ctc     633
255 Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp Leu Leu
256     180             185                 190
258 agc ttt aaa aga gga aat gcc ttg gag gag aaa gag aac aaa ata gtg     681
259 Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys Ile Val
260 195             200                 205                 210
262 gtg agg caa aca ggc tat ttc ttc atc tac agc cag gtt cta tac acg     729
263 Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr
264             215                 220                 225
266 gac ccc atc ttt gct atg ggt cat gtc atc cag agg aag aaa gta cac     777
267 Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His
268             230                 235                 240
270 gtc ttt ggg gac gag ctg agc ctg gtg acc ctg ttc cga tgt att cag     825
271 Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln
272     245             250                 255
274 aat atg ccc aaa aca ctg ccc aac aat tcc tgc tac ttg gct ggc atc     873
275 Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Leu Ala Gly Ile
276     260             265                 270
278 gcg agg ctg gaa gaa gga gat gag att cag ctt gca att cct cgg gag     921
279 Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu
280 275             280                 285                 290
282 aat gca cag att tca cgc aac gga gac gac acc ttc ttt ggt gcc cta     969
283 Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu
284             295                 300                 305
286 aaa ctg ctg taactcactt gctggagtgc gtgatcccct tccctcgtct           1018
287 Lys Leu Leu
290 tctctgtacc tccgagggag aaacagacga ctggaaaaat aaaagatggg gaaagccgtc  1078
292 agcgaaagtt ttctcgtgac ccgttgaatc tgatccaaac caggaaatat aacagacagc  1138
294 c                                                                  1139
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/779,050

DATE: 03/07/2001
TIME: 11:03:02

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

```
297 <210> SEQ ID NO: 4
298 <211> LENGTH: 309
299 <212> TYPE: PRT
300 <213> ORGANISM: Mus musculus
302 <400> SEQUENCE: 4
304 Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
305 1               5                   10                  15
308 Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
309             20                  25                  30
312 Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
313         35                  40                  45
316 Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
317     50                  55                  60
320 Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
321 65                  70                  75                  80
324 Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
325                 85                  90                  95
328 Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
329             100                 105                 110
332 Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
333         115                 120                 125
336 Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
337     130                 135                 140
340 Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
341 145                 150                 155                 160
344 Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
345                 165                 170                 175
348 Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp
349             180                 185                 190
352 Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys
353         195                 200                 205
356 Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu
357     210                 215                 220
360 Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys
361 225                 230                 235                 240
364 Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys
365                 245                 250                 255
368 Ile Gln Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Leu Ala
369                 260                 265                 270
372 Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro
373         275                 280                 285
376 Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly
377     290                 295                 300
380 Ala Leu Lys Leu Leu
381 305
384 <210> SEQ ID NO: 5
385 <211> LENGTH: 278
386 <212> TYPE: PRT
387 <213> ORGANISM: Homo sapiens
```

(see item 6 on Error Summary Sheet)

```
<210>   5
<211>   278
<212>   PRT
<213>   Homo sapiens

<220>
<221>   misc_feature
<223>   X = one or more naturally occurring amino acid residues.
```

This implies variable length, which is not permitted.

Xaa can only represent a single amino acid

```
<400>   5

Met Asp Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Cys
1               5                   10                  15

Xaa Xaa Lys Xaa Glu Xaa Met Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20          25                  30

Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Gly Xaa Leu
        35                  40                  45

Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Xaa Xaa Xaa Thr Xaa
    50                  55                  60

Xaa Ser Xaa Tyr Gln Xaa Ala Ala Leu Gln Xaa Asp Leu Xaa Xaa Leu
65              70                  75                  80

Arg Xaa Glu Leu Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Ala Xaa Ala
            85                  90                  95

Gly Ala Pro Xaa Xaa Thr Ala Gly Xaa Lys Xaa Xaa Xaa Pro Xaa Ala
            100                 105                 110

Pro Xaa Xaa Xaa Asn Ser Ser Xaa Xaa Xaa Arg Asn Xaa Arg Ala Xaa
        115                 120                 125

Gln Gly Pro Glu Glu Thr Xaa Xaa Gln Asp Cys Leu Gln Leu Ile Ala
    130                 135                 140

Asp Ser Xaa Thr Pro Thr Ile Xaa Lys Gly Xaa Tyr Thr Phe Val Pro
145                 150                 155                 160

Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn
                165                 170                 175

Lys Ile Xaa Val Xaa Xaa Thr Gly Tyr Phe Phe Ile Tyr Xaa Gln Val
            180                 185                 190

Leu Tyr Thr Asp Xaa Xaa Xaa Ala Met Gly His Xaa Ile Gln Arg Lys
            195                 200                 205

Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg
    210                 215                 220

Cys Ile Gln Asn Met Pro Xaa Thr Leu Pro Asn Asn Ser Cys Tyr Ser
225                 230                 235                 240
```

(partial listing of seq. 5)

Please ensure all sequences with this error are corrected.

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:396 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:396 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:399 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:402 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:405 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:408 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:411 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:414 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:417 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:420 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:423 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:429 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:432 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:438 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:441 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:444 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:462 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:462 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:465 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:468 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:471 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:474 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:477 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1156 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1156 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1159 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:1177 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1177 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1199 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1199 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1202 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
M:340 Repeated in SeqNo=27
L:1205 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1208 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1211 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1217 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1220 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1223 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
```